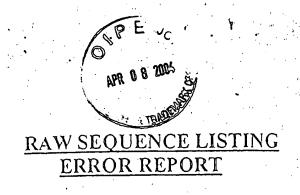
WE SON THE STATE OF THE SECOND	Application No.	Applicant(s)
otice to Complectived	09/068,377	LASKY ET AL.
, of Rotice to Commerce Wed	Examiner	Art Unit
NOTICE O COMPLY WITH REQUIREMENTS	Stephen L. Rawlings, Ph.D.	1642
NOTICE TO COMPLY WITH REQUIREMENTS	S FOR PATENT APPLICAT	IONS CONTAINING
NUCLEOTIDE SEQUENCEHOOD DREAMINGS	ACID SEQUENCE DISCLO	SURES
Applicant must file the items indicated below within the ti avoid abandonment under 35 U.S.C. § 133 (extensions of		
The nucleotide and/or amino acid sequence disclosure c for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.8		not comply with the requirements
1. This application clearly fails to comply with the req directed to the final rulemaking notice published at 5 the effective filing date is on or after July 1, 1998, see 1998) and 1211 OG 82 (June 23, 1998).	5 FR 18230 (May 1, 1990), and 1	114 OG 29 (May 15, 1990). If
<ul> <li>2. This application does not contain, as a separate p required by 37 C.F.R. 1.821(c).</li> </ul>	art of the disclosure on paper cop	y, a "Sequence Listing" as
3. A copy of the "Sequence Listing" in computer read 37 C.F.R. 1.821(e).	lable form has not been submitted	d as required by
4. A copy of the "Sequence Listing" in computer reaccomputer readable form does not comply with the reattached copy of the marked -up "Raw Sequence Listing".	quirements of 37 C.F.R. 1.822 an	
5. The computer readable form that has been filed w unreadable as indicated on the attached CRF Disket submitted as required by 37 C.F.R. 1.825(d).		
☐ 6. The paper copy of the "Sequence Listing" is not the as required by 37 C.F.R. 1.821(e).	e same as the computer readable	e from of the "Sequence Listing"
☐ 7. Other:		
Applicant Must Provide:  ☑ An initial or substitute computer readable form (CRF	) copy of the "Sequence Listing".	
An initial or substitute paper copy of the "Sequence specification.	Listing", as well as an amendmen	t directing its entry into the
A statement that the content of the paper and comp no new matter, as required by 37 C.F.R. 1.821(e) or 1.8		
For questions regarding compliance to these re	equirements, please contact	:
For Rules Interpretation, call (703) 308-4216 For CRF Submission Help, call (703) 308-4212 Patentin Software Program Support		
Technical Assistance To Purchase Patentin Software		
PLEASE RETURN A COPY OF THIS NOTICE	WITH YOUR REPLY	





The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/068.3970
Source:	1 1600 -
Date Processed by STIC:	1/4/04~
	7-1

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two. 2011 South Clark Place, Arlington, VA 22202
- Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTW  Wrapped Nucleics Wrapped Aminos Wrapped Aminos Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line." This may occur if your file Wrapped Aminos The number tiext at the end of each line "wrapped" down to the next line." This may occur if your file Wrapped Aminos The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  **Non-ASCII The submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequents submission is saved in ASCII text.  **Sequence(s)  Contain n's or Xaa's sepresenting more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.  **A "bug" in Patentin version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)  Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.  **Skipped Sequences  Sequence(s)  missing. If intentional, please insert the fullowing times for each skipped sequence (OLD RULES)  (OLD RULES)  Normal Time that the fullowing times for each skipped sequence (OLD RULES)  **SEQUENCE DESCRIPTIONS:EQ-ID NO.X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences (NEW RULES)  New RULES)  Per 1.823 of Sequence Rules, the only vailed <213> responses to include the skipped sequence of acid number  400> sequence(s)  Per 1.823 of Sequence Rules, use of <220>-\$223> is MANDATORY if n's or Xaa's are present.		1010
Wrapped Nucleics Wrapped Aminos Wrapped Aminos Prevent "wrapping."  Invalid Line Length Wrapped Aminos Prevent "wrapping."  Invalid Line Length The numbering under each \$^8\$ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  Misaligned Amino Numbering The numbering under each \$^8\$ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  Non-ASCII  The submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please each or or Xa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <200-<222> section that some may be missing.  Palentin 2.0  A "bug" in Patentin version 2.0 has coused the <2200-<222> section that some may be missing. Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <2200-<222> section to the subsequent amino acid sequence. This applies to the mandatory <2200-<222> section for Artificial or Unknown sequences.  Skipped Sequences  Sequence(s) missing. If intentional, please insert the fullowing lines for each skipped sequence (OLD RULES)  (OLD RULES)  (NEW RULES)  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences (NEW RULES)  Response  Sequence(s) missing. If intentional, please insert the following lines for each skipped sequences (NEW RULES)  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences (NEW RULES)  Per 1.823 of Sequence Rules, use of <2200-\$223> is MANDATORY if n's or Xaa's are present. In <2200 to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent Use of <2200 to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent "Unknown." Please of Sequence (of genetic matterial in <2200 to <223> recipients of Sequence (of genetic matterial in <2200 to <223> recipients	ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/068,3770
Wrapped Aminos was retrieved in a word processor after creating it. "Picase adjust your right margin to .3; this will prevent "wrapping."  Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.  Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  The submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.  The submitted file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Per Sequence Per Sequence Please and indicate in the \$220> \$223> section to be missing from amino acid sequence. Per Sequence Please Rules Rules Per Sequence Please Rules Rules Per Sequence Please Rules Rules Per Sequence Rules Ru	ATTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY 12TO SOFTWAR
Misaligned Amino Numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.  The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.  The submitted file was not saved in ASC		was retrieved in a word processor after creating il. Psease adjust your right margin to .3; this will
Numbering use space characters, instead.  4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please rensure your subsequent submission is saved in ASCII text.  5 Variable Length Sequence(s) Sequence(s) Sequence Rules, acan not saved in ASCII text.  6 Paientin 2.0 The submitted file was not saved in ASCII text.  6 Paientin 2.0 The submitted file was not saved in ASCII text.  6 Paientin 2.0 A "bug" in Patentin version 2.0 has caused the <220> <223> section to be missing from amino acid sequence. Please generally expert the file some may be missing.  7 Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220> <223> section to the subsequent amino acid sequence. This applies to the mandatory <220> <223> sections for Artificial or Unknown sequences.  7 Skipped Sequences (OLD RULES) (OLD RULES) (I) INFORMATION FOR SEQ ID NO.X: (insert SEQ ID NO where "X" is shown) (I) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO.X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences (NEW RULES) (NEW RULES) (NEW RULES) (NEW RULES)  10 Invalid <213> Per 1.823 of Sequence Rules, use of <220> *220> *222> is MANDATORY if n's or Xaa's are present. In <220> to <223> section if required when <213> response is Unknown is Artificial Sequence  11 Use of <220> Sequence(s)  12 Patentin 2.0  Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
Scapence   Sequence	·	
Sequence(s) contain n's or Xaa's representials more than one residue. Per Sequence Rules, each nor Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.  A "bug" in Patentln version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences. Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> sections for Artificial or Unknown sequences.  Sequence(s) missing. If intentional, please insent the fullowing lines for each skipped sequence (OLD RULES) (2) INFORMATION FOR SEQ ID NO.X: (insent SEQ ID NO where "X" is shown)  This sequence DESCRIPTION:SEQ.ID NO.X: (insent SEQ ID NO where "X" is shown)  This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences (NEW RULES)  Sequence(s) missing. If intentional, please insent the following lines for each skipped sequences (NEW RULES)  Use of n's or Xaa's  Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence of the complete of the comp	. 4 Non-ASCII	ensure your subsequent submission is saved in ASCII text.
"bug" sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.  7 Skipped Sequences (OLD RULES) (2) INFORMATION FOR SEQ ID NO.X: (insert SEQ ID No where "X" is shown) (3) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ.ID NO.X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences (NEW RULES) (NEW RULES)  Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (NEW RULES)  Use of n's or Xaa's (NEW RULES)  Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-8223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent  10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence. Or "Unknown." Please explain source of genetic material in <220> to <223> to <223> is MANDATORY if <213> "Organism" responsers "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> to <220> to <223> is MANDATORY if <213> "Organism" responsers "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 0001/1998, Vol. 63, No104, pp. 29631-32) (Sec. 1.823 of Sequence Rule "Please do not use "Côpy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequen	SVariable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each
(OLD RULES) (2) INFORMATION FOR SEQ ID NO.X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO.X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences  (NEW RULES)  Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (NEW RULES)  Use of n's or Xaa's (NEW RULES)  Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>.223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent.  Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence  Use of <220> to <222> missing the <220> "Feature" and associated numeric identifiers and responses Use of <220> to <223> is MANDATORY if <213> "Organism" responser's "Artificial Sequence" or "Unknown." Please explain source of genetic material in <200 to <223> section. (See "Federal Register," 0001/1998, Vol. 63, No104, pp. 29631-32) (Sec. 1.823 of Sequence Rule  Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	· ———	sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Skipped Sequences (NEW RULES)  Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (NEW RULES)  Use of n's or Xaa's (NEW RULES)  Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220> 2223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent Response  Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220> <223> section is required when <213> response is Unknown is Artificial Sequence  Use of <220> to <223> is MANDATORY if <213> "Organism" responsers "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00701/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules is under the control of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ.ID NO:X: (insert SEQ ID NO where "X" is shown)
(NEW RULES)    Vise of n's or Xaa's   Use of n's and/or Xaa's have been dereted in the Sequence Listing.		Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
NEW RULES    Per 1.823 of Sequence Rules, use of <220> \$\frac{2}{2}23>\$ is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent. In <220>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220> <220> <223> section is required when <213> response is Unknown is Artificial Sequence.   One of <220>   Sequence(s)   Please of <220>   Teature and associated numeric identifiers and responses use of <220>   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules are resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.		<210> sequence id number <400> sequence id number
Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknow is Artificial Sequence  Sequence(s)		Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220> \$\frac{1}{223}\$ is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 00701/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rule Patentin 2.0  "bug"  Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.		Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	11Use of <220>	Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid		resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
	13 Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/068,377D

DATE: 01/04/2004

TIME: 13:06:58

180

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Output Set: N:\CRF4\01042004\I068377D.raw

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        Dowbenko, Donald J.
9 <120> TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated
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12 <130> FILE REFERENCE: P1066P2
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14 <140> CURRENT APPLICATION NUMBER: US 09/068,377D
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24 <151> PRIOR FILING DATE: 1997-02-07
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                                         40
43 Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
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58 Ala Ile Met Asp Arg Val Gln Lys Ser Lys Leu Ser Leu Tyr Lys
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175

170

RAW SEQUENCE LISTING DATE: 01/04/2004 PATENT APPLICATION: US/09/068,377D TIME: 13:06:58

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140. ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gctccttcct 450
142 _catttcgctg ctgattctag ccccaaacaa aacaggttga gcctttttcc 500
    tecteeggea gttgeetetg gettgtgget geettetgag egttteagae 550
     ggcgccggct gggagtggga gggagggcct gggctagccg cgctgggact 600
```

RAW SEQUENCE LISTING DATE: 01/04/2004

PATENT APPLICATION: US/09/068,377D TIME: 13:06:58

Input Set : A:\P1066P2.txt

Output Set: N:\CRF4\01042004\I068377D.raw

```
gggacgtgct cctggctcct ggcccatgct cagccctgct tgaagcagga 650
150
    gtgctagcat ttgacacaac gcccttggag gatgatggcc cagctgcagt 700
152
    tccgagatgc cttctggtgc agggacttca cggcccacac agggtatgag 750
154
    gtgctactgc agaggctgct ggacggcagg aagatgtgca aggatgtgga 800
    ggagctgctc agacagaggg cccaggcgga ggagaggtac gggaaggagc 850
    tggtgcagat tgcacgcaag gctggtggcc agacagagat gaattccctg 900
    aggacetect ttgacteect gaageageaa acagagaatg tgggcagtge 950
162 acacatccag ctggccctgg ccctgcgtga ggagctgcgg agcctggagg 1000
    agttccgaga gagacagaaa gagcagcgga agaagtatga ggccatcatg 1050
164
    gaccgtgtcc agaagagcaa gttgtcgctc tacaagaaga ccatggagtc 1100
166
168
    caagaaggca tatgaccaga agtgcaggga tgcagatgat gctgagcagg 1150
170
    ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
172
    cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
174
    gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300
176
    aggageaccg gactacctgt gaggeettee agttgeagga gtttgaecgg 1350
178
    ctcaccatcc tccgcaatgc cctgtgggtg cactgtaacc agctctccat 1400
180
    gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450
182
    agggctgtga tgtggaaggt gacatcaatg gcttcatcca gtccaagagc 1500
184 actggcagag agcccccagc tccggtgcct tatcagaact actatgacag 1550
186 qqaqqtqacc ccactgattq gcaqccctaq catccaqccc tcctqcqqtq 1600
    tgataaagag gttctctggg ctgctacatg gaagtcccaa gaccacacct 1650
190 tetgeteetg etgetteeae agagaetetg acteceaece etgageggaa 1700
192 tgagttggtc tacgcatcca tcgaagtgca ggcgacccag ggaaacctta 1750
    acteateage ceaggactae egggeactet acgaetaeae tgeacagaat 1800
194
    tetgatgage tggacattte egegggagae ateetggegg teateetgga 1850
196
198
    aggggaggat ggctggtgga ctgtggagcg gaacggacaa cgtggctttg 1900
200
    teeetgggte gtaettggag aagetetgag gaaaggetag eagteteeae 1950
202
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     caggeeteae ggggeeagaa eeaageeegg tggtgetggg catgggetgg 2050
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209 <211> LENGTH: 48
210 <212> TYPE: PRT
211 <213> ORGANISM: Mus Musculus
213 <400> SEQUENCE: 3
     Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser
215
217
    Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
218
                      20 ·
                                         25
                                                             30
220
     Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
221
223
    Tyr Leu Arg
226 <210> SEO ID NO: 4
227 <211> LENGTH: 50
228 <212> TYPE: PRT
229 <213> ORGANISM: Homo sapien
231 <400> SEQUENCE: 4
    Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
233
                                                             15
```

RAW SEQUENCE LISTING DATE: 01/04/2004 PATENT APPLICATION: US/09/068,377D TIME: 13:06:58

Input Set : A:\P1066P2.txt

Output Set: N:\CRF4\01042004\1068377D.raw

```
235 Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
236
                      20
                                        . 25
238 Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
239
                     . 35
241 Tyr Val Glu Lys Ile
242
244 <210> SEQ ID NO: 5
245 <211> LENGTH: 50
246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapien
249 <400> SEQUENCE: 5
250 Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
251
       1
                                          10
253 Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
254
                      20
                                          25
256 Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
257
                      35
259 Tyr Val Lys Lys Leu
260
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 50
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapien
267 <400> SEQUENCE: 6
    Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
268
269
     - 1
                                                 15
                                          10
271 Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
272
                      20
                                          25
274 Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
275
                      35
                                         40
277
     Tyr Val Lys Leu Leu
278
280 <210> SEQ ID NO: 7
281 <211> LENGTH: 48
282 <212> TYPE: PRT
283 <213> ORGANISM: Homo sapien
285 <400> SEQUENCE: 7
. 286 Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
287
                                         10
289 Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
290
                      20
                                          25
292 Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
293
                      35
295 Tyr Val Glu
298 <210> SEQ ID NO: 8
 299 <211> LENGTH: 8
 300 <212> TYPE: PRT
 301 <213> ORGANISM: Artificial Sequence
 303 <220> FEATURE:
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RAW SEQUENCE LISTING DATE: 01/04/2004 PATENT APPLICATION: US/09/068,377D TIME: 13:06:58

Input Set : A:\P1066P2.txt ;

Output Set: N:\CRF4\01042004\I068377D.raw

304 <223> OTHER INFORMATION: Amino acid epitope tag 306 <400> SEQUENCE: 8 307 Asp Tyr Lys Asp Asp Asp Lys 308 1 310 <210> SEQ ID NO: 9 311 <211> LENGTH: 33 312 <212> TYPE: DNA 313 <213> ORGANISM: Artificial Sequence 315 <220> FEATURE: 316 <223> OTHER INFORMATION: Synthetic oligonucleotide probe 318 <400> SEQUENCE: 9 319 egeggateca ceatgatgge ceagetgeag tte 33 321 <210> SEQ ID NO: 10 322 <211> LENGTH: 45 323 <212> TYPE: DNA 324 <213> ORGANISM: Artificial Sequence 326 <220> FEATURE: 327 <223> OTHER INFORMATION: Synthetic oligonucleotide probe 329 <400> SEQUENCE: 10 330 gtacgcgtcg actcacttgt catcgtcgtc cttgtagtcg agctt 45 332 <210> SEQ ID NO: 11 333 <211> LENGTH: 18 334 <212> TYPE: DNA 335 <213> ORGANISM: Artificial Sequence 337 <220> FEATURE: 338 <223> OTHER INFORMATION: Synthetic oligonucleotide probe 340 <400> SEQUENCE: 11 341 tgcctttctc tccacagg 18 343 <210> SEQ ID NO: 12 344 <211> LENGTH: 36 345 <212> TYPE: DNA 346 <213> ORGANISM: Artificial Sequence 348 <220> FEATURE: 349 <223> OTHER INFORMATION: Synthetic oligonucleotide probe 351 <400> SEQUENCE: 12 352 ctccttgagg ttctactagt gggggctggt gtcctg 36 354 <210> SEQ ID NO: 13 355 <211> LENGTH: 39 356 <212> TYPE: DNA 357 <213> ORGANISM: Artificial Sequence: 359 <220> FEATURE: 360 <223> OTHER INFORMATION: Synthetic oligonucleotide probe 362 <400> SEQUENCE: 13 363 geggeegeac tagtatecag tetgtgetee atetgttae 39 365 <210> SEQ ID NO: 14 366 <211> LENGTH: 17 367 <212> TYPE: DNA 368 <213> ORGANISM: Artificial Sequence

370 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/068,377D

DATE: 01/04/2004 TIME: 13:06:59

Input Set : A:\P1066P2.txt

(see p.7)

Output Set: N:\CRF4\01042004\I068377D.raw

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:27; Xaa Pos. 2,3

2210> SEQ ID NO 27 sel ten/1 on Evor Surmary Sheet	• • • • • • • • • • • • • • • • • • • •
2212> TYPE: PRT	٠
COLON ODGINITON DANISSINIA COMMINA	
2213> ORGANISM: AFCITICIAI Sequence 2220> FEATURE: 2223> OTHER INFORMATION: Any amino acid this does not Uplain' 2400> SEQUENCE: 27 Pro (Xaa Xaa) Pro  Artificial Sequence	,
223> OTHER INFORMATION: Any amino acid	• .
:400> SEQUENCE: 27	Price
Pro(Xaa Xaa)Pro	•
1	÷.
T. noe -	• .
-the hold grilaining (P.6)	

VERIFICATION SUMMARY ...

PATENT APPLICATION: US/09/068,377D

DATE: 01/04/2004

TIME: 13:06:59

Input Set : A:\P1066P2.txt

Output Set: N:\CRF4\01042004\I068377D.raw

L:711 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:27 L:711 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:27

L:711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0